

SEQUENCE LISTING

<110> Istituto Di Ricerche Di Biologia Molecolare P. Angeletti S.P.A.

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND
USES THEREOF

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<150> 60/635,791

<151> 2004-12-14

<150> 60/543,649

<151> 2004-02-11

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acgccgttca atgtcgaga ggggaggag gtgcTTCTAC ttgtccacaa tctgccccag 180
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aacaatcaga gcctcccggt cagtcccagg ctgcagctgt ccaatggcaa caggaccctc 600
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cccaagccct	ccatctccag	caacaactcc	aaacccgtgg	aggacaagga	tgctgtggcc	1560
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aatgaggaga	cccagaatct	gagcacaata	tatctcagga	aatatcaatc	aaaagttaa	2700
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<211> 921
<212> PRT
<213> Artificial Sequence
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<220>
<223> CEA-LTB fusion

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Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
   35          40          45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
   50          55          60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
   65          70          75          80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
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 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
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 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
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 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
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 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
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 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
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 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
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 Thr Val Ser Ala Ser Gly Thr Leu Val Asn Gly Asp Lys Leu Tyr Arg
 675 680 685
 Ala Asp Ser Arg Pro Pro Asp Glu Ile Lys Arg Ser Gly Gly Leu Met
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 Pro Arg Gly His Asn Glu Tyr Phe Asp Arg Gly Thr Gln Met Asn Ile
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 Asn Leu Tyr Asp His Ala Arg Gly Thr Gln Thr Gly Phe Val Arg Tyr
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 Ala Gly Gln Ser Ile Leu Ser Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val
 755 760 765
 Ile Ala Thr Ala Pro Asn Met Phe Asn Val Asn Asp Val Leu Gly Val
 770 775 780
 Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu Gly Gly Ile
 785 790 795 800
 Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe Gly Val Ile
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 Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg
 820 825 830
 Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu Ala Gly Phe
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 Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile His His Ala
 850 855 860
 Pro Gln Gly Cys Gly Asn Ser Ser Arg Thr Ile Thr Asp Asp Thr Cys
 865 870 875 880
 Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg Lys Tyr Gln
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 <212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

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<223> CEA-LTB fusion

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35 40 45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
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Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145 150 155 160
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Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
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Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
210 215 220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225 230 235 240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
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Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
260 265 270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
275 280 285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
290 295 300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305 310 315 320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
325 330 335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
340 345 350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
355 360 365
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Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
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Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
420 425 430

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 740 745 750
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEAopt-LTB fusion

<400> 11

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 accCTGCAcG tgatCAAGAG cgacCTGGTG aacGAGGAGG CCACCGGCCA GTTCCGCGTG 420
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 aacaACCAGA gcCTGCCGT gagCCCCCGC CTGAGCTGA gcaacGGCAA CGCACCCTG 600
 accCTGTTCA acgtGACCCG caacGACACC GCGAGCTACA agtGCGAGAC CGAGAACCCC 660
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 accCAGGAGC tggTCATCCC caacATCACC GTGAACAACA GCGGCAGCTA CACCTGCCAG 900
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 ataaATGACA AGATACTATC ATATAcGGAA TCGATGGCAG GCAAAAGAGA AATGGTTATC 2160
 attACATTa AGAGCGGCCA AACATTTCAG GTCGAAGTCC CGGGCAGTCA ACATATAGAC 2220
 tcccAGAAAAA AAGCATTGA AAGGATGAAG GACACATTAA GAATCACATA TCTGACCGAG 2280
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 <211> 2358
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEAopt-LTBopt fusion

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 cacCTGTTG gctacagCTG gtacaAGGGC gagCGCgtGG acggcaaccg ccagatcatc 240
 ggctacGTGA tcggCACCCA gcaggCCACC CCCGGCCCCG CCTACAGCGG CGCGAGATC 300

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gacggcggtgg cttcacctg cgagccccgag acccaggagcg ccacctacct gtgggtgggtg 540
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<210> 13

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 13

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Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
50 55 60

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
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 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
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 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
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 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
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 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
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 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
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 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
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 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
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 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
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 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Ala Pro Gln Ser Ile Thr Glu
 675 680 685
 Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
 690 695 700
 Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
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 725 730 735
 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
 740 745 750
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 <211> 2358
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> rhCEAopt-LTBopt fusion

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<211> 784

<212> PBT

<213> Artificial Semience

5220>

<223> rhCEAopt-LTBopt fusion

<400> 15

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 130 135 140
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 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
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Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
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 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
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 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
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 675 680 685
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 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
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 <211> 2118
 <212> DNA
 <213> Macaca mulatta

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 <212> DNA
 <213> Macaca mulatta

<400> 17

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 <212> PRT
 <213> Macaca mulatta

<400> 18

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	20									25					30
Thr	Ala	Gln	Leu	Thr	Ile	Glu	Ser	Arg	Pro	Phe	Asn	Val	Ala	Glu	Gly
		35				40									45
Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly
		50				55									60
Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly
	65				70				75						80
Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser
		85							90						95
Gly	Arg	Glu	Thr	Ile	Asp	Phe	Asn	Ala	Ser	Leu	Leu	Ile	His	Asn	Val
	100				105										110
Thr	Gln	Ser	Asp	Thr	Gly	Ser	Tyr	Thr	Ile	Gln	Val	Ile	Lys	Glu	Asp
	115				120				125						
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
	130				135				140						
Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	Asp	Lys
	145				150				155						160
Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr	Thr	Tyr
		165						170							175
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Glu
		180				185									190
Leu	Ser	Ser	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	Arg	Asn
	195					200									205
Asp	Thr	Thr	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Val	Arg
	210				215				220						
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	225				230				235						240
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn	Leu	Asn
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Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
	275				280				285						
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Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val	Tyr	Ala
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 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
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 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
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 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
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 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
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 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
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 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
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 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
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 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
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 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
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 Met
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<210> 19
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 <212> PRT

<213> Macaca mulatta

<400> 19

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Thr	Ala	Gln	Leu	Leu	Thr	Ile	Glu	Ser	Arg	Pro	Phe	Asn	Val	Ala	Glu	Gly
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Lys	Glu	Val	Leu	Leu	Leu	Ala	His	Asn	Val	Ser	Gln	Asn	Leu	Phe	Gly	
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Tyr	Ile	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Ala	Ser	Arg	Arg	Ile	Gly	
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Ser	Cys	Val	Ile	Arg	Thr	Gln	Gln	Ile	Thr	Pro	Gly	Pro	Ala	His	Ser	
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Gly	Arg	Glu	Thr	Ile	Asp	Phe	Asn	Ala	Ser	Leu	Leu	Ile	His	Asn	Val	
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Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Ile	Glu	
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Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr	
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Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser	Ser	Arg	
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Leu	Glu	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro	
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Val	Arg	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	
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Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
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 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
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 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
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 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Asn Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
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 675 680 685
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 Met
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
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 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
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 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Ile Thr Val Tyr Ala
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 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
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 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
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 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
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 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
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 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495

Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
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 580 585 590
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 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
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 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
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<211> 679

<212> PRT

<213> Artificial Sequence

<220>

<223> deleted human CEA

<400> 23

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Lys	Glu	Val	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly	
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Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
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 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
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 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
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 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
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 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
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Phe Ile Ala Lys Ile Thr Pro Asn Asn Gly Thr Tyr Ala Cys Phe
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<213> Artificial Sequence

<220>
<223> CEA-FRC fusion

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<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 25

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<212> DNA

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<223> CEA-LAMP fusion

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<210> 27

<211> 3921

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-HSP70 fusion

<400> 27

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 gagattgacg gcaagaataa caccgcgccc gagatcagcg cccgcattct gatgaagctg 2340
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 aacgtgctgc ggatcgtaa cgagccgacc gcccgcgcg tggctacgg cctcgacaag 2520
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<210> 28
 <211> 3585
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA-VSVG fusion

<400> 28

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 acgcccgttca atgtcgcaga gggaaaggag gtgcttctac ttgtccacaa tctgccccag 180
 catcttttttgcgtacagctg gtacaaaaggat gaaagagtgg atggcaacccg tcaaattata 240
 ggatatgtaa taggaactca acaagctacc ccaggccccg catacagtgg tcgagagata 300
 atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
 accctacacg tcataaaagtc agatcttgcg aatgaagaag caactggcca gttccgggt 420
 taccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccctgt ggaggacaag 480
 gatgctgtgg cttcacctg tgaacctgag actcaggacg caacctacct gtgggtgggt 540
 aacaatcaga gcctcccggt cagtcggcagg ctgcagctgt ccaatggcaa caggaccctc 600
 actctattca atgtcacaag aatgacacaca gcaagctaca aatgtgaaac ccagaaccca 660

gtgagtgccca ggccgcagtga ttcaagtcatc ctgaatgtcc tctatggccc ggatgcccccc 720
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 gcagcctcta acccacctgc acagtaactt tggttgtca atggacttt ccagcaatcc 840
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 gttgaccaca gcgacccagt catcctgaat gtcctctatg gcccagacga ccccaccatt 1260
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 aactcagcca gtggccacag caggactaca gtcaagacaa tcacagtctc tgcggagctg 1500
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 ccagactcgt cttacctttc gggagcgaac ctcacacctt cctgcccactc ggcctctaac 1860
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 agaatggtcg gaatgatcgtt tggaaactacc acagaaagggg aactgtggga tgactgggt 3180
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 ctattcttgg ttctccgagt tggatattat ctttacatttta aattaaagca caccaagaaa 3540
 agacagattt atacagacat agagatgaac cgacttggaa ggtaa 3585

<210> 29
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
<223> PCR primer

<400> 29
tattctagat tcaacaccaa ttccattttc ttattc 36

<210> 30
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 30
gcggccgcta gaatcatttg tccatccttc atc 33

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 31
tattctagat tcaacaccaa ttccattttc ttattc 36

<210> 32
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 32
tttagcgccg ctagttctgt atcatatcgt aaaggg 36

<210> 33
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 33
tctagataaa actcacacat gcccc 25

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 34
gccgactcat ttacccggag acagggag 28

<210> 35
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 35
tctagatttg atccccattg ctgtgggcgg tgccctg 37

<210> 36
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 36
ggcgtgactc ctcttcctgc caatgaggta ggcaatgag 39

<210> 37
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 37
atatcttagat ttcaccatag tttttccaca caacc 35

<210> 38
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 38
gcggccgcct tccttccaag tcggttcatc tctatg 36

<210> 39
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 39
gctctagata tggctcgtgc ggtcgggatc gacc 34

<210> 40
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 40
gccgcggccg ctcacttggc ctccccggccg tcgtcg 36

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 41
gttatctaga agcaccccca tccc 24

<210> 42
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 42
ttaagatctc taagatctgg tgtcgtatct cagggg 36

<210> 43
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 43
ttatctagaa agacccacac ctgccccct tgc 33

<210> 44
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
 <223> PCR primer

<400> 44
 tatagatctt agggcacctt acttgccggg g

31

<210> 45
 <211> 952
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-Dom fusion

<400> 45
 Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
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 Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
 20 25 30 .
 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45 .
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60 .
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80 .
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95 .
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110 .
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125 .
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140 .
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160 .
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175 .
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190 .
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205 .
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220 .
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240 .
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255 .
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270 .
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285 .
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300 .
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
 305 310 315 320 .

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Ser Thr Pro Ile Pro Phe Ser
 675 680 685
 Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp
 690 695 700
 Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp
 705 710 715 720
 Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro
 725 730 735
 Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val
 740 745 750

Asn	Asn	Glu	Ser	Ser	Glu	Val	Ile	Val	His	Lys	Ala	Met	Asp	Ile	Glu
755					760							765			
Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val
770					775							780			
Pro	Lys	Val	Ser	Ala	Ser	His	Leu	Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr
785					790					795			800		
Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys	His	Ser	Leu	Ser	Ile	Gly	Ser	Gly
					805					810			815		
Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn	Asn	Leu	Ile	Trp	Thr	Leu	Lys	Asp
					820					825			830		
Ser	Ala	Gly	Glu	Val	Arg	Gln	Ile	Thr	Phe	Arg	Asp	Leu	Pro	Asp	Lys
					835				840			845			
Phe	Asn	Ala	Tyr	Leu	Ala	Asn	Lys	Trp	Val	Phe	Ile	Thr	Ile	Thr	Asn
					850				855			860			
Asp	Arg	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	Ile	Asn	Gly	Val	Leu	Met	Gly
					865				870			875			880
Ser	Ala	Glu	Ile	Thr	Gly	Leu	Gly	Ala	Ile	Arg	Glu	Asp	Asn	Asn	Ile
					885				890			895			
Thr	Leu	Lys	Leu	Asp	Arg	Cys	Asn	Asn	Asn	Gln	Tyr	Val	Ser	Ile	
					900				905			910			
Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys	Ala	Leu	Asn	Pro	Lys	Glu	Ile	Glu
					915				920			925			
Lys	Leu	Tyr	Thr	Ser	Tyr	Leu	Ser	Ile	Thr	Phe	Leu	Arg	Asp	Phe	Trp
					930				935			940			
Gly	Asn	Pro	Leu	Arg	Tyr	Asp	Thr								
					945				950						

<210> 46
<211> 907
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA-FcIgG fusion

<400>	46														
Met	Glu	Ser	Pro	Ser	Ala	Pro	Pro	His	Arg	Trp	Cys	Ile	Pro	Trp	Gln
1					5				10				15		
Arg	Leu	Leu	Leu	Thr	Ala	Ser	Leu	Leu	Thr	Phe	Trp	Asn	Pro	Pro	Thr
					20				25				30		
Thr	Ala	Lys	Leu	Thr	Ile	Glu	Ser	Thr	Pro	Phe	Asn	Val	Ala	Glu	Gly
					35				40				45		
Lys	Glu	Val	Leu	Leu	Leu	Val	His	Asn	Leu	Pro	Gln	His	Leu	Phe	Gly
					50				55				60		
Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
					65				70				75		80
Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
					85				90				95		
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
					100				105				110		
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
					115				120				125		

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Lys Thr His Thr Cys Pro Pro
 675 680 685
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 690 695 700
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 705 710 715 720
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 725 730 735
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 740 745 750
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 755 760 765
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 770 775 780
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 785 790 795 800
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 805 810 815
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 820 825 830
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 835 840 845
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 850 855 860
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 865 870 875 880
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 885 890 895
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 900 905

<210> 47
 <211> 825
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DOM

<400> 47

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 attatatcag atatatctgg gtttaattca tctgtataa cataatccaga tgctcaattg 180
 gtgcggaa taaatggcaa agcaatacat tttagtaaaca atgaatcttc tgaagttata 240
 gtgcataaag ctatggatataat gatatgttta ataattttac cgtagctt 300
 tggttgaggg ttccctaaagt atctgctagt catttagaac aatatggcac aaatgagtt 360
 tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctggttg gagtgatca 420
 cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 480
 acttttaggg atttacctga taaatttaat gcttatttag caaataaaatg gggtttata 540
 actattacta atgatagatt atcttctgct aatttgtata taaatggagt acttatggga 600
 agtgcagaaa ttactggttt aggagctatt agagaggata ataatataac attaaaacta 660
 gatagatgtata ataataataa tcaatacggt tctattgata aatttaggtat atttgcaaa 720
 gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aacctttta 780
 agagacttct gggaaaccc ttacgatata gatacagata ggttag 825

<210> 48

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> DOM

<400> 48

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Val	Asp	Asn	Glu	Glu	Asp	Ile	Asp	Val	Ile	Leu	Lys	Lys	Ser	Thr	Ile
	20														30
Leu	Asn	Leu	Asp	Ile	Asn	Asn	Asp	Ile	Ile	Ser	Asp	Ile	Ser	Gly	Phe
		35													45
Asn	Ser	Ser	Val	Ile	Thr	Tyr	Pro	Asp	Ala	Gln	Leu	Val	Pro	Gly	Ile
			50												60
Asn	Gly	Lys	Ala	Ile	His	Leu	Val	Asn	Asn	Glu	Ser	Ser	Glu	Val	Ile
	65														80
Val	His	Lys	Ala	Met	Asp	Ile	Glu	Tyr	Asn	Asp	Met	Phe	Asn	Asn	Phe
				85											95
Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro	Lys	Val	Ser	Ala	Ser	His	Leu
				100											110
Glu	Gln	Tyr	Gly	Thr	Asn	Glu	Tyr	Ser	Ile	Ile	Ser	Ser	Met	Lys	Lys
		115													125
His	Ser	Leu	Ser	Ile	Gly	Ser	Gly	Trp	Ser	Val	Ser	Leu	Lys	Gly	Asn
		130													140
Asn	Leu	Ile	Trp	Thr	Leu	Lys	Asp	Ser	Ala	Gly	Glu	Val	Arg	Gln	Ile
		145													160
Thr	Phe	Arg	Asp	Leu	Pro	Asp	Lys	Phe	Asn	Ala	Tyr	Leu	Ala	Asn	Lys
				165											175
Trp	Val	Phe	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Ser	Ser	Ala	Asn	Leu
				180											190
Tyr	Ile	Asn	Gly	Val	Leu	Met	Gly	Ser	Ala	Glu	Ile	Thr	Gly	Leu	Gly
		195													205
Ala	Ile	Arg	Glu	Asp	Asn	Asn	Ile	Thr	Leu	Lys	Leu	Asp	Arg	Cys	Asn
		210													220
Asn	Asn	Asn	Gln	Tyr	Val	Ser	Ile	Asp	Lys	Phe	Arg	Ile	Phe	Cys	Lys
		225													240

Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu Tyr Thr Ser Tyr Leu Ser
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 Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
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 Asp Arg

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<210> 49
<211> 2857
<212> DNA
<213> Artificial Sequence
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<220>
<223> CEA-DOM fusion

<400> 49
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ggatatgtaa taggaactca acaagctacc ccagggcccc catacagtgg tcgagagata 300
atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
accctacacg tcataaaagtc agatcttgc aatgaagaag caactggcca gttccggta 420
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccctg ggaggacaag 480
gatgctgtgg cttcacctg tgaacctgag actcaggacg caacctacat gtgggtggta 540
aacaatcaga gcctcccggt cagttccagg ctgcagctgt ccaatggcaa caggaccctc 600
actctattca atgtcacaag aaatgacaca gcaagctaca aatgtgaaac ccagaaccca 660
gtgagtgcca ggcgcagtga ttcaagtcat ctgaatgtcc tctatggccc ghatggcccc 720
accattttcc ctctaaacac atcttacaga tcagggggaaa atctgaacct ctcctgcccac 780
gcagccctcta accccacctgc acagttactt tggtttgtca atggacttt ccagcaatcc 840
acccaagagc tctttatccc caacatcaact gtgaataata gtggatccta tacgtccaa 900
gcccataact cagacactgg cctcaatagg accacagtcg cgacgatcac agtctatgca 960
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gttgaccaca gcgaccctgt catcctgaat gtcctctatg gcccgacga cccaccatt 1260
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 gatagatgta ataataataa tcaatacgtt tctattgata aatttaggtat atttgcaaa 2760
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<210> 50

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 50

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 cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
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 gacagatgca acaacaacaa ccagtacgtg agcatcgaca agttccggat cttctgcaag 2760
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<210> 51
 <211> 952
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> rhCEA-DOMopt fusion

<400> 51
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 Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
 50 55 60
 Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
 65 70 75 80
 Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
 85 90 95
 Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100 105 110
 Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240

Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
 500 505 510
 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670

Ser Val Ser Ser Gly Asp Ser Ser Arg Ser Thr Pro Ile Pro Phe Ser
 675 680 685
 Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp
 690 695 700
 Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp
 705 710 715 720
 Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro
 725 730 735
 Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val
 740 745 750
 Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu
 755 760 765
 Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
 770 775 780
 Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr
 785 790 795 800
 Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly
 805 810 815
 Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp
 820 825 830
 Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys
 835 840 845
 Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn
 850 855 860
 Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly
 865 870 875 880
 Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile
 885 890 895
 Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile
 900 905 910
 Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu
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 Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp
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 Gly Asn Pro Leu Arg Tyr Asp Thr
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<210> 52
 <211> 2359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> rhCEA-CTB^{opt} fusion

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gacggccgtgg ccctgacctg cgagccccgag acccaggaca ccacacctt gtgggggtg 540
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gtgagcgtgc gccgcagcga cccctgtgacc ctgaacgtgc tgtacggccc cgaccccccc 720
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agccagaaga aggccatcga gcggatgaag gacaccctgc ggatcgccta cctcaccggag 2280
gccaagggtgg agaagctgtg cgtgtggaaac aacaagaccc ctcacgccat cgccggccatc 2340
agcatggcca attgataag 2359

<210> 53
<211> 784
<212> PRT
<213> Artificial Sequence

<220>
<223> rhCEA-CTB₀pt fusion

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<400> 53
Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
   1           5           10          15
Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
   20          25          30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
   35          40          45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
   50          55          60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
   65          70          75          80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
   85          90          95

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Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100 105 110
 Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
 500 505 510
 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
 515 520 525

Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
 Ser Val Ser Ser Gly Asp Ser Ser Arg Thr Pro Gln Asn Ile Thr Asp
 675 680 685
 Leu Cys Ala Glu Tyr His Asn Thr Gln Ile Tyr Thr Leu Asn Asp Lys
 690 695 700
 Ile Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile
 705 710 715 720
 Ile Thr Phe Lys Asn Gly Ala Ile Phe Gln Val Glu Val Pro Gly Ser
 725 730 735
 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
 740 745 750
 Leu Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val
 755 760 765
 Trp Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 770 775 780

<210> 54
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> tetanus toxoid peptide

<400> 54
 Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala
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 Ser His Leu Glu
 20